

(1) GENERAL INFORMATION:

- (i) APPLICANT: Maertens, Geert  
Bosman, Fons  
De Martynoff, Guy  
Buyse, Marie-Ange
- (ii) TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.
- (iii) NUMBER OF SEQUENCES: 122
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: NIXON & VANDERHYE
  - (B) STREET: 1100 North Glebe Road, 8th Floor
  - (C) CITY: Arlington, VA 22201
  - (E) COUNTRY: USA
  - (F) ZIP: 22201
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: Unassigned
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Sadoff, B. J.
  - (B) REGISTRATION NUMBER: 36653
  - (C) REFERENCE/DOCKET NUMBER: 2551-61
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (703) 816-4000
  - (B) TELEFAX: (703) 816-4100

## (2) INFORMATION FOR SEQ ID NO: 1:

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 21 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCATGCAAG CTTAATTAAT T

21

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 68 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT  
TAACTGCA

60

68

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 642 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..639

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT | 48  |
| Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys |     |
| 1 5 10 15                                                       |     |
| CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG | 96  |
| Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met |     |
| 20 25 30                                                        |     |
| TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA | 144 |
| Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala |     |

| 35                                                                                                                                                    | 40 | 45 |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|----|----|-----|
| GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG<br>Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu<br>50 55 60        |    |    | 192 |
| AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT<br>Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala<br>65 70 75 80     |    |    | 240 |
| AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG<br>Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu<br>85 90 95        |    |    | 288 |
| CTC GTT GGG GCG GCT GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC<br>Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu<br>100 105 110     |    |    | 336 |
| TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC<br>Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg<br>115 120 125     |    |    | 384 |
| CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC<br>Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His<br>130 135 140     |    |    | 432 |
| ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT<br>Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro<br>145 150 155 160 |    |    | 480 |
| ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC<br>Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val<br>165 170 175     |    |    | 528 |
| GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC<br>Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala<br>180 185 190     |    |    | 576 |
| TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA<br>Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu<br>195 200 205     |    |    | 624 |
| CTC TTT GCT CTC TAATAG<br>Leu Phe Ala Leu<br>210                                                                                                      |    |    | 642 |

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val | Ser | Gly | Met |

| 20  |     |     |     |     |     |     |     |     |     | 25  |     |     |     |     |     |  |  |  |  | 30 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys | Val | Arg | Glu |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr | Leu | Ala | Ala |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | Val | Asp | Leu |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu | Val | Gly | Ala | Ala | Ala | Leu | Cys | Ser | Ala | Met | Tyr | Val | Gly | Asp | Leu |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp | Ser | Pro |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Thr | Thr | Ala | Leu | Val | Val | Ser | Gln | Leu | Leu | Arg | Ile | Pro | Gln | Ala | Val |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala | Gly | Leu | Ala |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Ile | Val | Met | Leu |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu | Phe | Ala | Leu |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 795 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..792

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..789

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | TTG | GGT | AAG | GTC | ATC | GAT | ACC | CTT | ACA | TGC | GGC | TTC | GCC | GAC | CTC | 48  |
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| GTG | GGG | TAC | ATT | CCG | CTC | GTC | GGC | GCC | CCC | CTA | GGG | GGC | GCT | GCC | AGG | 96  |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAG | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| ACA | GGG | AAT | TTG | CCC | GGT | TGC | TCT | TTC | TCT | ATC | TTC | CTC | TTG | GCT | TTG | 192 |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CTG | TCC | TGT | CTG | ACC | GTT | CCA | GCT | TCC | GCT | TAT | GAA | GTG | CGC | AAC | GTG | 240 |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| TCC | GGG | ATG | TAC | CAT | GTC | ACG | AAC | GAC | TGC | TCC | AAC | TCA | AGC | ATT | GTG | 288 |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| TAT | GAG | GCA | GCG | GAC | ATG | ATC | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGC | 336 |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| GTT | CGG | GAG | AAC | AAC | TCT | TCC | CGC | TGC | TGG | GTA | GCG | CTC | ACC | CCC | ACG | 384 |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| CTC | GCA | GCT | AGG | AAC | GCC | AGC | GTC | CCC | ACC | ACG | ACA | ATA | CGA | CGC | CAC | 432 |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His |     |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| GTC | GAT | TTG | CTC | GTT | GGG | GCG | GCT | GCT | TTC | TGT | TCC | GCT | ATG | TAC | GTG | 480 |
| Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |     |
| GGG | GAC | CTC | TGC | GGA | TCT | GTC | TTC | CTC | GTC | TCC | CAG | CTG | TTC | ACC | ATC | 528 |
| Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| TCG | CCT | CGC | CGG | CAT | GAG | ACG | GTG | CAG | GAC | TGC | AAT | TGC | TCA | ATC | TAT | 576 |
| Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| CCC | GGC | CAC | ATA | ACG | GGT | CAC | CGT | ATG | GCT | TGG | GAT | ATG | ATG | ATG | AAC | 624 |
| Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| TGG | TCG | CCT | ACA | ACG | GCC | CTG | GTG | GTA | TCG | CAG | CTG | CTC | CGG | ATC | CCA | 672 |
| Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser | Gln | Leu | Leu | Arg | Ile | Pro |     |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| CAA | GCT | GTC | GTG | GAC | ATG | GTG | GCG | GGG | GCC | CAT | TGG | GGA | GTC | CTG | GCG | 720 |
| Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |     |
| GGT | CTC | GCC | TAC | TAT | TCC | ATG | GTG | GGG | AAC | TGG | GCT | AAG | GTT | TTG | ATT | 768 |

Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile  
 245 250 255

GTG ATG CTA CTC TTT GCT CCC TAATAG  
 Val Met Leu Leu Phe Ala Pro  
 260

795

## (2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 263 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
 1 5 10 15  
 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
 20 25 30  
 Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala  
 35 40 45  
 Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu  
 50 55 60  
 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val  
 65 70 75 80  
 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val  
 85 90 95  
 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys  
 100 105 110  
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125  
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140  
 Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val  
 145 150 155 160  
 Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile  
 165 170 175  
 Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr  
 180 185 190  
 Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn  
 195 200 205  
 Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
 210 215 220  
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala

(2) INFORMATION FOR SEO ID NO: 7:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..630

(ix) FEATURE:

```
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..627
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | TTG | GGT | AAG | GTC | ATC | GAT | ACC | CTT | ACG | TGC | GGC | TTC | GCC | GAC | CTC | 48  |
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| ATG | GGG | TAC | ATT | CCG | CTC | GTC | GGC | GCC | CCC | CTA | GGG | GGT | GCT | GCC | AGA | 96  |
| Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAA | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| ACA | GGG | AAT | TTG | CCT | GGT | TGC | TCT | TTC | TCT | ATC | PTC | CTC | TTG | GCT | TTA | 192 |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CTG | TCC | TGT | CTG | ACC | ATT | CCA | GCT | TCC | GCT | TAT | GAG | GTG | CGC | AAC | GTG | 240 |
| Leu | Ser | Cys | Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| TCC | GGG | ATG | TAC | CAT | GTC | ACG | AAC | GAC | TGC | TCC | AAC | TCA | AGC | ATT | GTG | 288 |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| TAT | GAG | GCA | GCG | GAC | ATG | ATC | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGC | 336 |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |

(2) INFORMATION FOR SEO ID NO: 8:

(A) LENGTH: 209 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ser | Cys | Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |



Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val  
 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile  
 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr  
 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn  
 195 200 205

Trp

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 483 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..480

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT | 48  |
| Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys |     |
| 1 5 10 15                                                       |     |
| CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG | 96  |
| Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val |     |
| 20 25 30                                                        |     |
| TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA | 144 |
| Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala |     |
| 35 40 45                                                        |     |
| GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG | 192 |
| Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu |     |
| 50 55 60                                                        |     |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC    | 240 |
| Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala    |     |
| 65 70 75 80                                                        |     |
| AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG    | 288 |
| Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu    |     |
| 85 90 95                                                           |     |
| CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC    | 336 |
| Leu Val Gly Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu        |     |
| 100 105 110                                                        |     |
| TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC    | 384 |
| Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg    |     |
| 115 120 125                                                        |     |
| CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT    | 432 |
| Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His    |     |
| 130 135 140                                                        |     |
| GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TCC TAATAG | 483 |
| Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser        |     |
| 145 150 155 160                                                    |     |

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys |  |
| 1 5 10 15                                                       |  |
| Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val |  |
| 20 25 30                                                        |  |
| Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala |  |
| 35 40 45                                                        |  |
| Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu |  |
| 50 55 60                                                        |  |
| Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala |  |
| 65 70 75 80                                                     |  |
| Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu |  |
| 85 90 95                                                        |  |
| Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu |  |
| 100 105 110                                                     |  |
| Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg |  |
| 115 120 125                                                     |  |
| Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 130 |     | 135 |     | 140 |     |     |     |     |     |     |     |     |     |     |
| Val | Ser | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..477

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..474

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | TCC | GGT | TGC | TCT | TTC | TCT | ATC | TTC | CTC | TTG | GCC | CTG | CTG | TCC | TGT | 48  |
| Met | Ser | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| CTG | ACC | ATA | CCA | GCT | TCC | GCT | TAT | GAA | GTG | CGC | AAC | GTG | TCC | GGG | GTG | 96  |
| Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val | Ser | Gly | Val |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| TAC | CAT | GTC | ACG | AAC | GAC | TGC | TCC | AAC | TCA | AGC | ATA | GTG | TAT | GAG | GCA | 144 |
| Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
| GCG | GAC | ATG | ATC | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGC | GTT | CGG | GAG | 192 |
| Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys | Val | Arg | Glu |     |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |     |
| GGC | AAC | TCC | TCC | CGT | TGC | TGG | GTG | GCG | CTC | ACT | CCC | ACG | CTC | GCG | GCC | 240 |
| Gly | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr | Leu | Ala | Ala |     |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |     |
| AGG | AAC | GCC | AGC | GTC | CCC | ACA | ACG | ACA | ATA | CGA | CGC | CAC | GTC | GAT | TTG | 288 |
| Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | Val | Asp | Leu |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| CTC | GTT | GGG | GCT | GCT | GCT | TTC | TGT | TCC | GCT | ATG | TAC | GTG | GGG | GAT | CTC | 336 |
| Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val | Gly | Asp | Leu |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| TGC | GGA | TCT | GTT | TTC | CTT | GTT | TCC | CAG | CTG | TTC | ACC | TTC | TCA | CCT | CGC | 384 |
| Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Phe | Ser | Pro | Arg |     |

(2) INFORMATION FOR SEQ ID NO: 12:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

(2) INFORMATION FOR SEO ID NO: 13:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | CTG | GGT | AAG | GCC | ATC | GAT | ACC | CTT | ACG | TGC | GGC | TTC | GCC | GAC | CTC | 48  |
| Met | Leu | Gly | Lys | Ala | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| GTG | GGG | TAC | ATT | CCG | CTC | GTC | GGC | GCC | CCC | CTA | GGG | GGC | GCT | GCC | AGG | 96  |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAA | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| ACA | GGG | AAT | TTG | CCT | GGT | TGC | TCT | TTC | TCT | ATC | TTC | CTC | TTG | GCT | TTA | 192 |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CTG | TCC | TGT | CTA | ACC | ATT | CCA | GCT | TCC | GCT | TAC | GAG | GTG | CGC | AAC | GTG | 240 |
| Leu | Ser | Cys | Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| TCC | GGG | ATG | TAC | CAT | GTC | ACG | AAC | GAC | TGC | TCC | AAC | TCA | AGC | ATT | GTG | 288 |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| TAT | GAG | GCA | GCG | GAC | ATG | ATC | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGC | 336 |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| GTT | CGG | GAG | AAC | AAC | TCT | TCC | CGC | TGC | TGG | GTA | GCG | CTC | ACC | CCC | ACG | 384 |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| CTC | GCG | GCT | AGG | AAC | GCC | AGC | ATC | CCC | ACT | ACA | ACA | ATA | CGA | CGC | CAC | 432 |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Ile | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His |     |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| GTC | GAT | TTG | CTC | GTT | GGG | GCG | GCT | GCT | TTC | TGT | TCC | GCT | ATG | TAC | GTG | 480 |
| Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| GGG | GAT | CTC | TGC | GGA | TCT | GTC | TTC | CTC | GTC | TCC | CAG | CTG | TTC | ACC | ATC | 528 |
| Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| TCG | CCT | CGC | CGG | CAT | GAG | ACG | GTG | CAG | GAC | TGC | AAT | TGC | TCA | ATC | TAT | 576 |
| Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr |     |

|                                                                 |     |  |     |  |     |     |
|-----------------------------------------------------------------|-----|--|-----|--|-----|-----|
|                                                                 | 180 |  | 185 |  | 190 |     |
| CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC |     |  |     |  |     | 624 |
| Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn |     |  |     |  |     |     |
|                                                                 | 195 |  | 200 |  | 205 |     |
| TGG TAC TAATAG                                                  |     |  |     |  |     | 640 |
| Trp Tyr                                                         |     |  |     |  |     |     |
| 210                                                             |     |  |     |  |     |     |

## (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Ala | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ser | Cys | Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Ile | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |







- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 723 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..720
- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC | 48  |
| Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu |     |
| 1 5 10 15                                                       |     |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG | 96  |
| Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg |     |
| 20 25 30                                                        |     |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA | 144 |
| Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala |     |
| 35 40 45                                                        |     |
| ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG | 192 |
| Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu |     |
| 50 55 60                                                        |     |
| CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG | 240 |
| Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val |     |
| 65 70 75 80                                                     |     |
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG | 288 |
| Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val |     |
| 85 90 95                                                        |     |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC | 336 |
| Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys |     |
| 100 105 110                                                     |     |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG | 384 |
| Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr |     |
| 115 120 125                                                     |     |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC | 432 |
| Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His     |     |
| 130 135 140                                                     |     |
| GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG | 480 |
| Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val |     |

|                                                                    |     |     |     |     |
|--------------------------------------------------------------------|-----|-----|-----|-----|
| 145                                                                | 150 | 155 | 160 |     |
| CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT    |     |     |     | 528 |
| Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg    | 165 | 170 | 175 |     |
| ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG    |     |     |     | 576 |
| Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val    | 180 | 185 | 190 |     |
| GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG    |     |     |     | 624 |
| Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala    | 195 | 200 | 205 |     |
| GGG GCC CAT TGG GGA GTC CTG GCG GGT CTC GCC TAC TAT TCC ATG GTG    |     |     |     | 672 |
| Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val    | 210 | 215 | 220 |     |
| GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC CTT GCT CCC TAATAG |     |     |     | 723 |
| Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro        | 225 | 230 | 235 | 240 |

## (2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Asp | Ser | Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val |

(2) INFORMATION FOR SEQ ID NO: 23:

(A) LENGTH: 561 base pairs

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..558

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..555

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | TTG | GGT | AAG | GTC | ATC | GAT | ACC | CTT | ACA | TGC | GGC | TTC | GCC | GAC | CTC | 48  |
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| GTG | GGG | TAC | ATT | CCG | CTC | GTC | GGC | GCC | CCC | CTA | GGG | GGC | GCT | GCC | AGG | 96  |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAG | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| ACA | GGG | AAT | TTG | CCC | GGT | TGC | TCT | TTC | TCT | ATC | TTC | CTC | TTG | GCT | TTG | 192 |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CTG | TCC | TGT | CTG | ACC | GTT | CCA | GCT | TCC | GCT | TAT | GAA | GTG | CGC | AAC | GTG | 240 |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |     |

| 65                                                              | 70  | 75  | 80  |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG |     |     |     | 288 |
| Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val | 85  | 90  | 95  |     |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC |     |     |     | 336 |
| Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys | 100 | 105 | 110 |     |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG |     |     |     | 384 |
| Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr | 115 | 120 | 125 |     |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC |     |     |     | 432 |
| Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His | 130 | 135 | 140 |     |
| GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG |     |     |     | 480 |
| Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val | 145 | 150 | 155 | 160 |
| CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT |     |     |     | 528 |
| Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg | 165 | 170 | 175 |     |
| ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG                      |     |     |     | 561 |
| Met Ala Trp Asp Met Met Met Asn Trp                             | 180 | 185 |     |     |

## (2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 185 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
|     | 20  |     |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val  
 145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg  
 165 170 175

Met Ala Trp Asp Met Met Met Asn Trp  
 180 185

## (2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 606 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..603

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..600

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC | 48  |
| Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu |     |
| 1 5 10 15                                                       |     |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG | 96  |
| Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg |     |
| 20 25 30                                                        |     |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA | 144 |
| Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala |     |
| 35 40 45                                                        |     |
| ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG | 192 |
| Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu |     |
| 50 55 60                                                        |     |
| CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG | 240 |
| Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val |     |
| 65 70 75 80                                                     |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG | 288 |
| Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val |     |
| 85 90 95                                                        |     |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC | 336 |
| Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys |     |
| 100 105 110                                                     |     |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG | 384 |
| Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr |     |
| 115 120 125                                                     |     |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC | 432 |
| Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His     |     |
| 130 135 140                                                     |     |
| GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG | 480 |
| Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val |     |
| 145 150 155 160                                                 |     |
| CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT | 528 |
| Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg |     |
| 165 170 175                                                     |     |
| ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG | 576 |
| Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val |     |
| 180 185 190                                                     |     |
| GTA TCG CAG CTG CTC CGG ATC CTC TAATAG                          | 606 |
| Val Ser Gln Leu Leu Arg Ile Leu                                 |     |
| 195 200                                                         |     |

## (2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
|     | 20  |     |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO: 27:

(ii) MOLECULE TYPE: cDNA.

(iii) ANTI-SENSE: NO

```
(ix) FEATURE:
      (A) NAME/KEY: mat_peptide
      (B) LOCATION: 1..630
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | TTG | GGT | AAG | GTC | ATC | GAT | ACC | CTT | ACA | TGC | GGC | TTC | GCC | GAC | CTC | 48  |
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GTG | GGG | TAC | ATT | CCG | CTC | GTC | GGC | GCC | CCC | CTA | GGG | GGC | GCT | GCC | AGG | 96  |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAG | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| ACA | GGG | AAT | TTG | CCC | GGT | TGC | TCT | TTC | TCT | ATC | TTC | CTC | TTG | GCT | TTG | 192 |

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu  
 50 55 60  
 CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG 240  
 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val  
 65 70 75 80  
 TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG 288  
 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val  
 85 90 95  
 TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC 336  
 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys  
 100 105 110  
 GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG 384  
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125  
 CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC 432  
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140  
 GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG 480  
 Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val  
 145 150 155 160  
 CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT 528  
 Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg  
 165 170 175  
 ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG 576  
 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val  
 180 185 190  
 GTA TCG CAG CTG CTC CGG ATC GTG ATC GAG GGC AGA CAC CAT CAC CAC 624  
 Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His His  
 195 200 205  
 CAT CAC TAATAG 636  
 His His  
 210

## (2) INFORMATION FOR SEQ ID NO: 28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
 1 5 10 15  
 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
 20 25 30  
 Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala



| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
|     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Val | Asp | Ser | Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr | Gly | His | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Ser | Gln | Leu | Leu | Arg | Ile | Val | Ile | Glu | Gly | Arg | His | His | His | His |
|     |     |     | 195 |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| His | His |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 630 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..627

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..624

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGA TTC GCC GAT CTC ATG

|        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met    | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu | Met |     |
| 1      |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| GGG    | TAC | ATC | CCG | CTC | GTC | GGC | GCT | CCC | GTA | GGA | GGC | GTC | GCA | AGA | GCC | 96  |
| Gly    | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Val | Gly | Gly | Val | Ala | Arg | Ala |     |
|        |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| CTT    | GCG | CAT | GGC | GTG | AGG | GCC | CTT | GAA | GAC | GGG | ATA | AAT | TTC | GCA | ACA | 144 |
| Leu    | Ala | His | Gly | Val | Arg | Ala | Leu | Glu | Asp | Gly | Ile | Asn | Phe | Ala | Thr |     |
|        |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| GGG    | AAT | TTG | CCC | GGT | TGC | TCC | TTT | TCT | ATT | TTC | CTT | CTC | GCT | CTG | TTC | 192 |
| Gly    | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu | Phe |     |
|        | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| TCT    | TGC | TTA | ATT | CAT | CCA | GCA | GCT | AGT | CTA | GAG | TGG | CGG | AAT | ACG | TCT | 240 |
| Ser    | Cys | Leu | Ile | His | Pro | Ala | Ala | Ser | Leu | Glu | Trp | Arg | Asn | Thr | Ser |     |
| 65     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| GGC    | CTC | TAT | GTC | CTT | ACC | AAC | GAC | TGT | TCC | AAT | AGC | AGT | ATT | GTG | TAC | 288 |
| Gly    | Leu | Tyr | Val | Leu | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val | Tyr |     |
|        |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| GAG    | GCC | GAT | GAC | GTT | ATT | CTG | CAC | ACA | CCC | GGC | TGC | ATA | CCT | TGT | GTC | 336 |
| Glu    | Ala | Asp | Asp | Val | Ile | Leu | His | Thr | Pro | Gly | Cys | Ile | Pro | Cys | Val |     |
|        |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |
| CAG    | GAC | GGC | AAT | ACA | TCC | ACG | TGC | TGG | ACC | CCA | GTG | ACA | CCT | ACA | GTG | 384 |
| Gln    | Asp | Gly | Asn | Thr | Ser | Thr | Cys | Trp | Thr | Pro | Val | Thr | Pro | Thr | Val |     |
|        | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| GCA    | GTC | AAG | TAC | GTC | GGA | GCA | ACC | ACC | GCT | TCG | ATA | CGC | AGT | CAT | GTG | 432 |
| Ala    | Val | Lys | Tyr | Val | Gly | Ala | Thr | Thr | Ala | Ser | Ile | Arg | Ser | His | Val |     |
|        | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| GAC    | CTA | TTA | GTG | GGC | GCG | GCC | ACG | ATG | TGC | TCT | GCG | CTC | TAC | GTG | GGT | 480 |
| Asp    | Leu | Leu | Val | Gly | Ala | Ala | Thr | Met | Cys | Ser | Ala | Leu | Tyr | Val | Gly |     |
| 145    |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |     |
| GAC    | ATG | TGT | GGG | GCT | GTC | TTC | CTC | GTG | GGA | CAA | GCC | TTC | ACG | TTC | AGA | 528 |
| Asp    | Met | Cys | Gly | Ala | Val | Phe | Leu | Val | Gly | Gln | Ala | Phe | Thr | Phe | Arg |     |
|        |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| CCT    | CGT | CGC | CAT | CAA | ACG | GTC | CAG | ACC | TGT | AAC | TGC | TCG | CTG | TAC | CCA | 576 |
| Pro    | Arg | Arg | His | Gln | Thr | Val | Gln | Thr | Cys | Asn | Cys | Ser | Leu | Tyr | Pro |     |
|        |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |
| GGC    | CAT | CTT | TCA | GGA | CAT | CGA | ATG | GCT | TGG | GAT | ATG | ATG | ATG | AAC | TGG | 624 |
| Gly    | His | Leu | Ser | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp |     |
|        | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| TAATAG |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 634 |

## (2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met  
 1 5 10 15

Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala  
 20 25 30

Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr  
 35 40 45

Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe  
 50 55 60

Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser  
 65 70 75 80

Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr  
 85 90 95

Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val  
 100 105 110

Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val  
 115 120 125

Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val  
 130 135 140

Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly  
 145 150 155 160

Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg  
 165 170 175

Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro  
 180 185 190

Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 630 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..627

## (ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..624

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC GCC GAT CTC ATG | 48  |
| Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met |     |
| 1 5 10 15                                                       |     |
| GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT GGG GGC GTC GCA AGG GCT | 96  |
| Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala |     |
| 20 25 30                                                        |     |
| CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA | 144 |
| Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr |     |
| 35 40 45                                                        |     |
| GGG AAT TTA CCC GGT TGC TCT TTC TCT ATC TTT ATT CTT GCT CTT CTC | 192 |
| Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu |     |
| 50 55 60                                                        |     |
| TCG TGT CTG ACC GTT CCG GCC TCT GCA GTT CCC TAC CGA AAT GCC TCT | 240 |
| Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser |     |
| 65 70 75 80                                                     |     |
| GGG ATT TAT CAT GTT ACC AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT | 288 |
| Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr |     |
| 85 90 95                                                        |     |
| GAG GCA GAT AAC CTG ATC CTA CAC GCA CCT GGT TGC GTG CCT TGT GTC | 336 |
| Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val |     |
| 100 105 110                                                     |     |
| ATG ACA GGT AAT GTG AGT AGA TGC TGG GTC CAA ATT ACC CCT ACA CTG | 384 |
| Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu |     |
| 115 120 125                                                     |     |
| TCA GCC CCG AGC CTC GGA GCA GTC ACG GCT CCT CTT CGG AGA GCC GTT | 432 |
| Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val |     |
| 130 135 140                                                     |     |
| GAC TAC CTA GCG GGA GGG GCT GCC CTC TGC TCC GCG TTA TAC GTA GGA | 480 |
| Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly |     |
| 145 150 155 160                                                 |     |
| GAC GCG TGT GGG GCA CTA TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG | 528 |
| Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg |     |
| 165 170 175                                                     |     |
| CCT CGC CAG CAC GCT ACG GTG CAG AAC TGC AAC TGT TCC ATT TAC AGT | 576 |
| Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser |     |
| 180 185 190                                                     |     |
| GGC CAT GTT ACC GGC CAC CGG ATG GCA TGG GAT ATG ATG ATG AAC TGG | 624 |
| Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp |     |
| 195 200 205                                                     |     |

TAATAG

630

## (2) INFORMATION FOR SEQ ID NO: 32:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1           5           10           15
Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala
          20           25           30
Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr
          35           40           45
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
          50           55           60
Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser
          65           70           75           80
Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr
          85           90           95
Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val
          100          105          110
Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu
          115          120          125
Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val
          130          135          140
Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly
          145          150          155          160
Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg
          165          170          175
Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser
          180          185          190
Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
          195          200          205

```

## (2) INFORMATION FOR SEQ ID NO: 33:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
 TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
 CTATTATGGT GGTAAGCCAC AGAGCAGGAG

30

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..1473

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
 TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG

48



|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| AAC<br>Asn | AAC<br>Asn | ACC<br>Thr | TTG<br>Leu | ACC<br>Thr | TGC<br>Cys | CCC<br>Pro | ACT<br>Thr | GAC<br>Asp | TGT<br>Cys | TTT<br>Phe | CGG<br>Arg | AAG<br>Lys | CAC<br>His | CCC<br>Pro | GAG<br>Glu | 816  |
|            |            |            | 260        |            |            |            |            | 265        |            |            |            |            | 270        |            |            |      |
| GCC<br>Ala | ACC<br>Thr | TAC<br>Tyr | GCC<br>Ala | AGA<br>Arg | TGC<br>Cys | GGT<br>Gly | TCT<br>Ser | GGG<br>Gly | CCC<br>Pro | TGG<br>Trp | CTG<br>Leu | ACA<br>Thr | CCT<br>Pro | AGG<br>Arg | TGT<br>Cys | 864  |
|            |            | 275        |            |            |            |            | 280        |            |            |            |            | 285        |            |            |            |      |
| ATG<br>Met | GTT<br>Val | CAT<br>His | TAC<br>Tyr | CCA<br>Pro | TAT<br>Tyr | AGG<br>Arg | CTC<br>Leu | TGG<br>Trp | CAC<br>His | TAC<br>Tyr | CCC<br>Pro | TGC<br>Cys | ACT<br>Thr | GTC<br>Val | AAC<br>Asn | 912  |
|            | 290        |            |            |            |            | 295        |            |            |            |            | 300        |            |            |            |            |      |
| TTC<br>Phe | ACC<br>Thr | ATC<br>Ile | TTC<br>Phe | AAG<br>Lys | GTT<br>Val | AGG<br>Arg | ATG<br>Met | TAC<br>Tyr | GTG<br>Val | GGG<br>Gly | GGC<br>Gly | GTG<br>Val | GAG<br>Glu | CAC<br>His | AGG<br>Arg | 960  |
| 305        |            |            |            |            | 310        |            |            |            |            | 315        |            |            |            |            | 320        |      |
| TTC<br>Phe | GAA<br>Glu | GCC<br>Ala | GCA<br>Ala | TGC<br>Cys | AAT<br>Asn | TGG<br>Trp | ACT<br>Thr | CGA<br>Arg | GGA<br>Gly | GAG<br>Glu | CGT<br>Arg | TGT<br>Cys | GAC<br>Asp | TTG<br>Leu | GAG<br>Glu | 1008 |
|            |            |            |            | 325        |            |            |            |            | 330        |            |            |            |            | 335        |            |      |
| GAC<br>Asp | AGG<br>Arg | GAT<br>Asp | AGA<br>Arg | TCA<br>Ser | GAG<br>Glu | CTT<br>Leu | AGC<br>Ser | CCG<br>Pro | CTG<br>Leu | CTG<br>Leu | CTG<br>Leu | TCT<br>Ser | ACA<br>Thr | ACA<br>Thr | GAG<br>Glu | 1056 |
|            |            |            | 340        |            |            |            |            | 345        |            |            |            |            | 350        |            |            |      |
| TGG<br>Trp | CAG<br>Gln | ATA<br>Ile | CTG<br>Leu | CCC<br>Pro | TGT<br>Cys | TCC<br>Ser | TTC<br>Phe | ACC<br>Thr | ACC<br>Thr | CTG<br>Leu | CCG<br>Pro | GCC<br>Ala | CTA<br>Leu | TCC<br>Ser | ACC<br>Thr | 1104 |
|            |            | 355        |            |            |            |            | 360        |            |            |            |            | 365        |            |            |            |      |
| GGC<br>Gly | CTG<br>Leu | ATC<br>Ile | CAC<br>His | CTC<br>Leu | CAT<br>His | CAG<br>Gln | AAC<br>Asn | ATC<br>Ile | GTG<br>Val | GAC<br>Asp | GTG<br>Val | CAA<br>Gln | TAC<br>Tyr | CTG<br>Leu | TAC<br>Tyr | 1152 |
|            | 370        |            |            |            |            | 375        |            |            |            |            | 380        |            |            |            |            |      |
| GGT<br>Gly | GTA<br>Val | GGG<br>Gly | TCG<br>Ser | GCG<br>Ala | GTT<br>Val | GTC<br>Val | TCC<br>Ser | CTT<br>Leu | GTC<br>Val | ATC<br>Ile | AAA<br>Lys | TGG<br>Trp | GAG<br>Glu | TAT<br>Tyr | GTC<br>Val | 1200 |
| 385        |            |            |            |            | 390        |            |            |            |            | 395        |            |            |            |            | 400        |      |
| CTG<br>Leu | TTG<br>Leu | CTC<br>Leu | TTC<br>Phe | CTT<br>Leu | CTC<br>Leu | CTG<br>Leu | GCA<br>Ala | GAC<br>Asp | GCG<br>Ala | CGC<br>Arg | ATC<br>Ile | TGC<br>Cys | GCC<br>Ala | TGC<br>Cys | TTA<br>Leu | 1248 |
|            |            |            |            | 405        |            |            |            |            | 410        |            |            |            | 415        |            |            |      |
| TGG<br>Trp | ATG<br>Met | ATG<br>Met | CTG<br>Leu | CTG<br>Leu | ATA<br>Ile | GCT<br>Ala | CAA<br>Gln | GCT<br>Ala | GAG<br>Glu | GCC<br>Ala | GCC<br>Ala | TTA<br>Leu | GAG<br>Glu | AAC<br>Asn | CTG<br>Leu | 1296 |
|            |            |            | 420        |            |            |            |            | 425        |            |            |            |            | 430        |            |            |      |
| GTG<br>Val | GTC<br>Val | CTC<br>Leu | AAT<br>Asn | GCG<br>Ala | GCG<br>Ala | GCC<br>Ala | GTG<br>Val | GCC<br>Ala | GGG<br>Gly | GCG<br>Ala | CAT<br>His | GGC<br>Gly | ACT<br>Thr | CTT<br>Leu | TCC<br>Ser | 1344 |
|            |            |            | 435        |            |            |            | 440        |            |            |            |            | 445        |            |            |            |      |
| TTC<br>Phe | CTT<br>Leu | GTG<br>Val | TTC<br>Phe | TTC<br>Phe | TGT<br>Cys | GCT<br>Ala | GCC<br>Ala | TGG<br>Trp | TAC<br>Tyr | ATC<br>Ile | AAG<br>Lys | GGC<br>Gly | AGG<br>Arg | CTG<br>Leu | GTC<br>Val | 1392 |
|            | 450        |            |            |            |            | 455        |            |            |            |            | 460        |            |            |            |            |      |
| CCT<br>Pro | GGT<br>Gly | GCG<br>Ala | GCA<br>Ala | TAC<br>Tyr | GCC<br>Ala | TTC<br>Phe | TAT<br>Tyr | GGC<br>Gly | GTG<br>Val | TGG<br>Trp | CCG<br>Pro | CTG<br>Leu | CTC<br>Leu | CTG<br>Leu | CTT<br>Leu | 1440 |
| 465        |            |            |            |            | 470        |            |            |            |            | 475        |            |            |            |            | 480        |      |
| CTG<br>Leu | CTG<br>Leu | GCC<br>Ala | TTA<br>Leu | CCA<br>Pro | CCA<br>Pro | CGA<br>Arg | GCT<br>Ala | TAT<br>Tyr | GCC<br>Ala | TAGTAA     |            |            |            |            |            | 1476 |
|            |            |            |            | 485        |            |            |            |            | 490        |            |            |            |            |            |            |      |





| 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr | Pro | Cys | Thr | Val | Asn |
| 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly | Gly | Val | Glu | His | Arg |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu | Arg | Cys | Asp | Leu | Glu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu | Leu | Ser | Thr | Thr | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Trp | Gln | Ile | Leu | Pro | Cys | Ser | Phe | Thr | Thr | Leu | Pro | Ala | Leu | Ser | Thr |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gly | Leu | Ile | His | Leu | His | Gln | Asn | Ile | Val | Asp | Val | Gln | Tyr | Leu | Tyr |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gly | Val | Gly | Ser | Ala | Val | Val | Ser | Leu | Val | Ile | Lys | Trp | Glu | Tyr | Val |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     | 400 |
| Leu | Leu | Leu | Phe | Leu | Leu | Leu | Ala | Asp | Ala | Arg | Ile | Cys | Ala | Cys | Leu |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Trp | Met | Met | Leu | Leu | Ile | Ala | Gln | Ala | Glu | Ala | Ala | Leu | Glu | Asn | Leu |
|     |     |     | 420 |     |     |     | 425 |     |     |     |     |     | 430 |     |     |
| Val | Val | Leu | Asn | Ala | Ala | Ala | Val | Ala | Gly | Ala | His | Gly | Thr | Leu | Ser |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Phe | Leu | Val | Phe | Phe | Cys | Ala | Ala | Trp | Tyr | Ile | Lys | Gly | Arg | Leu | Val |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Pro | Gly | Ala | Ala | Tyr | Ala | Phe | Tyr | Gly | Val | Trp | Pro | Leu | Leu | Leu | Leu |
| 465 |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |     |
| Leu | Leu | Ala | Leu | Pro | Pro | Arg | Ala | Tyr | Ala |     |     |     |     |     |     |
|     |     |     | 485 |     |     |     |     | 490 |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1021 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1018

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide



| 225                                                             | 230 | 235 |      |
|-----------------------------------------------------------------|-----|-----|------|
| TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC |     |     | 766  |
| Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr |     |     |      |
| 240                                                             | 245 | 250 | 255  |
| GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT |     |     | 814  |
| Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His |     |     |      |
|                                                                 | 260 | 265 | 270  |
| TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC |     |     | 862  |
| Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile |     |     |      |
|                                                                 | 275 | 280 | 285  |
| TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC |     |     | 910  |
| Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala |     |     |      |
|                                                                 | 290 | 295 | 300  |
| GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT |     |     | 958  |
| Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp |     |     |      |
|                                                                 | 305 | 310 | 315  |
| AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG TGG CAG AGT |     |     | 1006 |
| Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser |     |     |      |
|                                                                 | 320 | 325 | 330  |
| GGC AGA GCT TAATTA                                              |     |     | 1021 |
| Gly Arg Ala                                                     |     |     |      |

## (2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln  
 115 120 125  
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg  
 130 135 140  
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala  
 145 150 155 160  
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val  
 165 170 175  
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala  
 180 185 190  
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly  
 195 200 205  
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr  
 210 215 220  
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu  
 225 230 235 240  
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala  
 245 250 255  
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr  
 260 265 270  
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe  
 275 280 285  
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala  
 290 295 300  
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg  
 305 310 315 320  
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly  
 325 330 335  
 Arg Ala

## (2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1034 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:



|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG<br>Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys<br>210 215 220     | 670  |
| ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC<br>Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr<br>225 230 235     | 718  |
| TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC<br>Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr<br>240 245 250 255 | 766  |
| GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT<br>Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His<br>260 265 270     | 814  |
| TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC<br>Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile<br>275 280 285     | 862  |
| TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC<br>Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala<br>290 295 300     | 910  |
| GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT<br>Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp<br>305 310 315     | 958  |
| AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG<br>Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly<br>320 325 330 335 | 1006 |
| CAG ACA CCA TCA CCA CCA TCA CTA AT AG<br>Gln Thr Pro Ser Pro Pro Ser Leu<br>340                                                                       | 1034 |

## (2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 343 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr  
                                     85                                    90                                    95  
 Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly  
                                     100                                    105                                    110  
 Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln  
                                     115                                    120                                    125  
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg  
                                     130                                    135                                    140  
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala  
 145                                    150                                    155                                    160  
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val  
                                     165                                    170                                    175  
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala  
                                     180                                    185                                    190  
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly  
                                     195                                    200                                    205  
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr  
                                     210                                    215                                    220  
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu  
 225                                    230                                    235                                    240  
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala  
                                     245                                    250                                    255  
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr  
                                     260                                    265                                    270  
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe  
                                     275                                    280                                    285  
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala  
                                     290                                    295                                    300  
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg  
 305                                    310                                    315                                    320  
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln  
                                     325                                    330                                    335  
 Thr Pro Ser Pro Pro Ser Leu  
                                     340

## (2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO





|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC | 624 |
| Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile |     |
| 195 200 205                                                     |     |
| GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG | 672 |
| Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg |     |
| 210 215 220                                                     |     |
| AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG | 720 |
| Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu |     |
| 225 230 235 240                                                 |     |
| ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC | 768 |
| Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro |     |
| 245 250 255                                                     |     |
| TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC | 816 |
| Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly |     |
| 260 265 270                                                     |     |
| GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT | 864 |
| Val Glu His Arg Phe Glu Ala Cys Asn Trp Thr Arg Gly Glu Arg     |     |
| 275 280 285                                                     |     |
| TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG | 912 |
| Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu |     |
| 290 295 300                                                     |     |
| TCT ACA ACA GAG TGG CAG AGC TTA ATT AAT TAG                     | 945 |
| Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn                         |     |
| 305 310                                                         |     |

## (2) INFORMATION FOR SEQ ID NO: 42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala |  |
| 1 5 10 15                                                       |  |
| Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp |  |
| 20 25 30                                                        |  |
| Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile |  |
| 35 40 45                                                        |  |
| Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu |  |
| 50 55 60                                                        |  |
| Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr |  |
| 65 70 75 80                                                     |  |
| Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys |  |
| 85 90 95                                                        |  |

```

Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr
      100                      105                      110

Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro
      115                      120                      125

Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr
      130                      135                      140

Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly
      145                      150                      155                      160

Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu
      165                      170                      175

Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met
      180                      185                      190

Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile
      195                      200                      205

Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg
      210                      215                      220

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu
      225                      230                      235                      240

Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro
      245                      250                      255

Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly
      260                      265                      270

Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
      275                      280                      285

Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu
      290                      295                      300

Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn
      305                      310

```

## (2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 961 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..958

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Lys | His | Pro | Glu | Ala | Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | Leu |  |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |     |
| ACA | CCT | AGG | TGT | ATG | GTT | CAT | TAC | CCA | TAT | AGG | CTC | TGG | CAC | TAC | CCC |  | 768 |
| Thr | Pro | Arg | Cys | Met | Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr | Pro |  |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |     |
| TGC | ACT | GTC | AAC | TTC | ACC | ATC | TTC | AAG | GTT | AGG | ATG | TAC | GTG | GGG | GGC |  | 816 |
| Cys | Thr | Val | Asn | Phe | Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly | Gly |  |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |     |
| GTG | GAG | CAC | AGG | TTC | GAA | GCC | GCA | TGC | AAT | TGG | ACT | CGA | GGA | GAG | CGT |  | 864 |
| Val | Glu | His | Arg | Phe | Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu | Arg |  |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |     |
| TGT | GAC | TTG | GAG | GAC | AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG | CTG |  | 912 |
| Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu | Leu |  |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |     |
| TCT | ACA | ACA | GGT | GAT | CGA | GGG | CAG | ACA | CCA | TCA | CCA | CCA | TCA | CTA | A   |  | 958 |
| Ser | Thr | Thr | Gly | Asp | Arg | Gly | Gln | Thr | Pro | Ser | Pro | Pro | Ser | Leu |     |  |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |  |     |
| TAG |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  | 961 |

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe | Ala |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |  |
| Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp |  |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
| Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |
| Arg | Ser | Ile | Asp | Lys | Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr |  |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Glu | Pro | Asn | Ser | Ser | Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |  |
| Arg | Pro | Cys | Gly | Ile | Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr |  |  |

|         |                     |                 |                 |                     |
|---------|---------------------|-----------------|-----------------|---------------------|
| 130     |                     | 135             |                 | 140                 |
| Cys 145 | Phe Thr Pro Ser     | Pro Val Val Val | Gly Thr Thr     | Asp Arg Phe Gly 160 |
|         |                     | 150             | 155             |                     |
| Val 145 | Pro Thr Tyr Asn 165 | Trp Gly Ala Asn | Asp Ser Asp     | Val Leu Ile Leu 175 |
|         |                     | 180             | 185             | 190                 |
| Asn 145 | Asn Thr Arg Pro     | Pro Arg Gly     | Asn Trp Phe Gly | Cys Thr Trp Met     |
|         |                     | 200             | 205             |                     |
| Asn 145 | Gly Thr Gly Phe Thr | Lys Thr Cys Gly | Gly Pro Pro     | Cys Asn Ile         |
|         |                     | 215             | 220             |                     |
| Gly 145 | Gly Ala Gly Asn Asn | Thr Leu Thr Cys | Pro Thr Asp     | Cys Phe Arg         |
|         |                     | 230             | 235             |                     |
| Lys 145 | His Pro Glu Ala Thr | Tyr Ala Arg Cys | Gly Ser Gly     | Pro Trp Leu 240     |
|         |                     | 245             | 250             | 255                 |
| Thr 145 | Pro Arg Cys Met     | Val His Tyr Pro | Tyr Arg Leu Trp | His Tyr Pro         |
|         |                     | 260             | 265             | 270                 |
| Cys 145 | Thr Val Asn Phe Thr | Ile Phe Lys Val | Arg Met Tyr Val | Gly Gly             |
|         |                     | 275             | 280             | 285                 |
| Val 145 | Glu His Arg Phe Glu | Ala Ala Cys Asn | Trp Thr Arg     | Gly Glu Arg         |
|         |                     | 290             | 295             | 300                 |
| Cys 145 | Asp Leu Glu Asp Arg | Asp Arg Ser Glu | Leu Ser Pro     | Leu Leu Leu         |
|         |                     | 305             | 310             | 315                 |
| Ser 145 | Thr Thr Gly Asp Arg | Gly Gln Thr Pro | Ser Pro Pro     | Ser Leu             |

## (2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1395 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..1392

- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 1..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala | Gly | Leu | Ala | Tyr | Tyr |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| TCC | ATG | GTG | GGG | AAC | TGG | GCT | AAG | GTT | TTG | GTT | GTG | ATG | CTA | CTC | TTT | 96  |
| Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GCC | GGC | GTC | GAC | GGG | CAT | ACC | CGC | GTG | TCA | GGA | GGG | GCA | GCA | GCC | TCC | 144 |
| Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| GAT | ACC | AGG | GGC | CTT | GTG | TCC | CTC | TTT | AGC | CCC | GGG | TCG | GCT | CAG | AAA | 192 |
| Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| ATC | CAG | CTC | GTA | AAC | ACC | AAC | GGC | AGT | TGG | CAC | ATC | AAC | AGG | ACT | GCC | 240 |
| Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala |     |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| CTG | AAC | TGC | AAC | GAC | TCC | CTC | CAA | ACA | GGG | TTC | TTT | GCC | GCA | CTA | TTC | 288 |
| Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| TAC | AAA | CAC | AAA | TTC | AAC | TCG | TCT | GGA | TGC | CCA | GAG | CGC | TTG | GCC | AGC | 336 |
| Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| TGT | CGC | TCC | ATC | GAC | AAG | TTC | GCT | CAG | GGG | TGG | GGT | CCC | CTC | ACT | TAC | 384 |
| Cys | Arg | Ser | Ile | Asp | Lys | Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| ACT | GAG | CCT | AAC | AGC | TCG | GAC | CAG | AGG | CCC | TAC | TGC | TGG | CAC | TAC | GCG | 432 |
| Thr | Glu | Pro | Asn | Ser | Ser | Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| CCT | CGA | CCG | TGT | GGT | ATT | GTA | CCC | GCG | TCT | CAG | GTG | TGC | GGT | CCA | GTG | 480 |
| Pro | Arg | Pro | Cys | Gly | Ile | Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| TAT | TGC | TTC | ACC | CCG | AGC | CCT | GTT | GTG | GTG | GGG | ACG | ACC | GAT | CGG | TTT | 528 |
| Tyr | Cys | Phe | Thr | Pro | Ser | Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Phe |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| GGT | GTC | CCC | ACG | TAT | AAC | TGG | GGG | GCG | AAC | GAC | TCG | GAT | GTG | CTG | ATT | 576 |
| Gly | Val | Pro | Thr | Tyr | Asn | Trp | Gly | Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| CTC | AAC | AAC | ACG | CGG | CCG | CCG | CGA | GCG | AAC | TGG | TTC | GGC | TGT | ACA | TGG | 624 |
| Leu | Asn | Asn | Thr | Arg | Pro | Pro | Arg | Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp |     |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| ATG | AAT | GGC | ACT | GGG | TTC | ACC | AAG | ACG | TGT | GGG | GGC | CCC | CCG | TGC | AAC | 672 |
| Met | Asn | Gly | Thr | Gly | Phe | Thr | Lys | Thr | Cys | Gly | Gly | Pro | Pro | Cys | Asn |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| ATC | GGG | GGG | GCC | GGC | AAC | AAC | ACC | TTG | ACC | TGC | CCC | ACT | GAC | TGT | TTT | 720 |
| Ile | Gly | Gly | Ala | Gly | Asn | Asn | Thr | Leu | Thr | Cys | Pro | Thr | Asp | Cys | Phe |     |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| CGG | AAG | CAC | CCC | GAG | GCC | ACC | TAC | GCC | AGA | TGC | GGT | TCT | GGG | CCC | TGG | 768 |
| Arg | Lys | His | Pro | Glu | Ala | Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC    | 816  |
| Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr    |      |
| 260 265 270                                                        |      |
| CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG    | 864  |
| Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly    |      |
| 275 280 285                                                        |      |
| GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG    | 912  |
| Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu    |      |
| 290 295 300                                                        |      |
| CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG    | 960  |
| Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu    |      |
| 305 310 315 320                                                    |      |
| CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG    | 1008 |
| Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu    |      |
| 325 330 335                                                        |      |
| CCG GCC CTA TCC ACC GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC    | 1056 |
| Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp    |      |
| 340 345 350                                                        |      |
| GTG CAA TAC CTG TAC GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC    | 1104 |
| Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile    |      |
| 355 360 365                                                        |      |
| AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC    | 1152 |
| Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg    |      |
| 370 375 380                                                        |      |
| ATC TGC GCC TGC TTA TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC    | 1200 |
| Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala    |      |
| 385 390 395 400                                                    |      |
| GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG    | 1248 |
| Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala    |      |
| 405 410 415                                                        |      |
| CAT GGC ACT CTT TCC TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC    | 1296 |
| His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile    |      |
| 420 425 430                                                        |      |
| AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG    | 1344 |
| Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp    |      |
| 435 440 445                                                        |      |
| CCG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA | 1395 |
| Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala        |      |
| 450 455 460                                                        |      |

## (2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 463 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein





Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu  
 325 330 335  
 Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp  
 340 345 350  
 Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile  
 355 360 365  
 Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg  
 370 375 380  
 Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala  
 385 390 395 400  
 Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala  
 405 410 415  
 His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile  
 420 425 430  
 Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp  
 435 440 445  
 Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2082 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2079

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..2076

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC  
 Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
 1 5 10 15  
 GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG  
 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
 20 25 30

48

96





|     |     |     |     |        |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Trp | Thr | Arg | Gly | Glu    | Arg | Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu |      |  |
| 530 |     |     |     |        |     | 535 |     |     |     |     | 540 |     |     |     |     |      |  |
| CTT | AGC | CCG | CTG | CTG    | CTG | TCT | ACA | ACA | GAG | TGG | CAG | ATA | CTG | CCC | TGT | 1680 |  |
| Leu | Ser | Pro | Leu | Leu    | Leu | Ser | Thr | Thr | Glu | Trp | Gln | Ile | Leu | Pro | Cys |      |  |
| 545 |     |     |     |        | 550 |     |     |     |     | 555 |     |     |     |     | 560 |      |  |
| TCC | TTC | ACC | ACC | CTG    | CCG | GCC | CTA | TCC | ACC | GGC | CTG | ATC | CAC | CTC | CAT | 1728 |  |
| Ser | Phe | Thr | Thr | Leu    | Pro | Ala | Leu | Ser | Thr | Gly | Leu | Ile | His | Leu | His |      |  |
|     |     |     |     | 565    |     |     |     |     | 570 |     |     |     |     | 575 |     |      |  |
| CAG | AAC | ATC | GTG | GAC    | GTG | CAA | TAC | CTG | TAC | GGT | GTA | GGG | TCG | GCG | GTT | 1776 |  |
| Gln | Asn | Ile | Val | Asp    | Val | Gln | Tyr | Leu | Tyr | Gly | Val | Gly | Ser | Ala | Val |      |  |
|     |     |     | 580 |        |     |     |     | 585 |     |     |     |     | 590 |     |     |      |  |
| GTC | TCC | CTT | GTG | ATC    | AAA | TGG | GAG | TAT | GTC | CTG | TTG | CTC | TTC | CTT | CTC | 1824 |  |
| Val | Ser | Leu | Val | Ile    | Lys | Trp | Glu | Tyr | Val | Leu | Leu | Leu | Phe | Leu | Leu |      |  |
|     |     | 595 |     |        |     |     | 600 |     |     |     |     | 605 |     |     |     |      |  |
| CTG | GCA | GAC | GCG | CGC    | ATC | TGC | GCC | TGC | TTA | TGG | ATG | ATG | CTG | CTG | ATA | 1872 |  |
| Leu | Ala | Asp | Ala | Arg    | Ile | Cys | Ala | Cys | Leu | Trp | Met | Met | Leu | Leu | Ile |      |  |
|     | 610 |     |     |        |     | 615 |     |     |     |     | 620 |     |     |     |     |      |  |
| GCT | CAA | GCT | GAG | GCC    | GCC | TTA | GAG | AAC | CTG | GTG | GTC | CTC | AAT | GCG | GCG | 1920 |  |
| Ala | Gln | Ala | Glu | Ala    | Ala | Leu | Glu | Asn | Leu | Val | Val | Leu | Asn | Ala | Ala |      |  |
| 625 |     |     |     |        | 630 |     |     |     |     | 635 |     |     |     |     | 640 |      |  |
| GCC | GTG | GCC | GGG | GCG    | CAT | GGC | ACT | CTT | TCC | TTC | CTT | GTG | TTC | TTC | TGT | 1968 |  |
| Ala | Val | Ala | Gly | Ala    | His | Gly | Thr | Leu | Ser | Phe | Leu | Val | Phe | Phe | Cys |      |  |
|     |     |     |     | 645    |     |     |     |     | 650 |     |     |     |     | 655 |     |      |  |
| GCT | GCC | TGG | TAC | ATC    | AAG | GGC | AGG | CTG | GTC | CCT | GGT | GCG | GCA | TAC | GCC | 2016 |  |
| Ala | Ala | Trp | Tyr | Ile    | Lys | Gly | Arg | Leu | Val | Pro | Gly | Ala | Ala | Tyr | Ala |      |  |
|     |     |     | 660 |        |     |     |     | 665 |     |     |     |     | 670 |     |     |      |  |
| TTC | TAT | GGC | GTG | TGG    | CCG | CTG | CTC | CTG | CTT | CTG | CTG | GCC | TTA | CCA | CCA | 2064 |  |
| Phe | Tyr | Gly | Val | Trp    | Pro | Leu | Leu | Leu | Leu | Leu | Leu | Ala | Leu | Pro | Pro |      |  |
|     |     | 675 |     |        |     | 680 |     |     |     |     |     | 685 |     |     |     |      |  |
| CGA | GCT | TAT | GCC | TAGTAA |     |     |     |     |     |     |     |     |     |     |     | 2082 |  |
| Arg | Ala | Tyr | Ala |        |     |     |     |     |     |     |     |     |     |     |     |      |  |
|     |     |     | 690 |        |     |     |     |     |     |     |     |     |     |     |     |      |  |

## (2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 692 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |

| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser | Gln | Leu | Leu | Arg | Ile | Pro |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | Trp | His |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | Gly | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | Cys | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Arg | Leu | Ala | Ser | Cys | Arg | Ser | Ile | Asp | Lys | Phe | Ala | Gln | Gly | Trp |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Pro | Leu | Thr | Tyr | Thr | Glu | Pro | Asn | Ser | Ser | Asp | Gln | Arg | Pro | Tyr |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Cys | Trp | His | Tyr | Ala | Pro | Arg | Pro | Cys | Gly | Ile | Val | Pro | Ala | Ser |     |



## (2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2433 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2430

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..2427

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC | 48  |
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn |     |
| 1 5 10 15                                                       |     |
| CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT | 96  |
| Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly |     |
| 20 25 30                                                        |     |
| GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG | 144 |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala |     |
| 35 40 45                                                        |     |
| ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGG AGG CGA CAA CCT | 192 |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro |     |
| 50 55 60                                                        |     |
| ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG | 240 |
| Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly |     |
| 65 70 75 80                                                     |     |
| TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGG TGG GCA GGA TGG | 288 |
| Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp |     |
| 85 90 95                                                        |     |
| CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC | 336 |
| Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro |     |
| 100 105 110                                                     |     |
| CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC | 384 |
| Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys |     |
| 115 120 125                                                     |     |
| GGC TTC GCC GAC CTC GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA | 432 |
| Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu |     |
| 130 135 140                                                     |     |
| GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC | 480 |







|     |     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|-----|------|--|
| Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu    | Arg | Cys | Asp | Leu | Glu | Asp |      |  |
|     |     |     |     | 645 |     |     |     |     | 650    |     |     |     |     | 655 |     |      |  |
| AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG    | CTG | TCT | ACA | ACA | GAG | TGG | 2016 |  |
| Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu    | Leu | Ser | Thr | Thr | Glu | Trp |      |  |
|     |     |     | 660 |     |     |     |     | 665 |        |     |     |     |     | 670 |     |      |  |
| CAG | ATA | CTG | CCC | TGT | TCC | TTC | ACC | ACC | CTG    | CCG | GCC | CTA | TCC | ACC | GGC | 2064 |  |
| Gln | Ile | Leu | Pro | Cys | Ser | Phe | Thr | Thr | Leu    | Pro | Ala | Leu | Ser | Thr | Gly |      |  |
|     |     |     | 675 |     |     |     | 680 |     |        |     |     | 685 |     |     |     |      |  |
| CTG | ATC | CAC | CTC | CAT | CAG | AAC | ATC | GTG | GAC    | GTG | CAA | TAC | CTG | TAC | GGT | 2112 |  |
| Leu | Ile | His | Leu | His | Gln | Asn | Ile | Val | Asp    | Val | Gln | Tyr | Leu | Tyr | Gly |      |  |
|     |     |     | 690 |     |     | 695 |     |     |        |     | 700 |     |     |     |     |      |  |
| GTA | GGG | TCG | GCG | GTT | GTC | TCC | CTT | GTC | ATC    | AAA | TGG | GAG | TAT | GTC | CTG | 2160 |  |
| Val | Gly | Ser | Ala | Val | Val | Ser | Leu | Val | Ile    | Lys | Trp | Glu | Tyr | Val | Leu |      |  |
|     | 705 |     |     |     | 710 |     |     |     |        | 715 |     |     |     | 720 |     |      |  |
| TTG | CTC | TTC | CTT | CTC | CTG | GCA | GAC | GCG | CGC    | ATC | TGC | GCC | TGC | TTA | TGG | 2208 |  |
| Leu | Leu | Phe | Leu | Leu | Ala | Asp | Ala | Arg | Ile    | Cys | Ala | Cys | Leu | Trp |     |      |  |
|     |     |     |     | 725 |     |     |     | 730 |        |     |     |     |     | 735 |     |      |  |
| ATG | ATG | CTG | CTG | ATA | GCT | CAA | GCT | GAG | GCC    | GCC | TTA | GAG | AAC | CTG | GTG | 2256 |  |
| Met | Met | Leu | Leu | Ile | Ala | Gln | Ala | Gln | Ala    | Ala | Leu | Glu | Asn | Leu | Val |      |  |
|     |     |     |     | 740 |     |     |     | 745 |        |     |     |     | 750 |     |     |      |  |
| GTC | CTC | AAT | GCG | GCG | GCC | GTG | GCC | GGG | GCG    | CAT | GGC | ACT | CTT | TCC | TTC | 2304 |  |
| Val | Leu | Asn | Ala | Ala | Ala | Val | Ala | Gly | Ala    | His | Gly | Thr | Leu | Ser | Phe |      |  |
|     |     | 755 |     |     |     |     | 760 |     |        |     |     | 765 |     |     |     |      |  |
| CTT | GTG | TTC | TTC | TGT | GCT | GCC | TGG | TAC | ATC    | AAG | GGC | AGG | CTG | GTC | CCT | 2352 |  |
| Leu | Val | Phe | Phe | Cys | Ala | Ala | Trp | Tyr | Ile    | Lys | Gly | Arg | Leu | Val | Pro |      |  |
|     |     |     |     |     |     | 775 |     |     |        |     | 780 |     |     |     |     |      |  |
| GGT | GCG | GCA | TAC | GCC | TTC | TAT | GGC | GTG | TGG    | CCG | CTG | CTC | CTG | CTT | CTG | 2400 |  |
| Gly | Ala | Ala | Tyr | Ala | Phe | Tyr | Gly | Val | Trp    | Pro | Leu | Leu | Leu | Leu | Leu |      |  |
|     | 785 |     |     |     | 790 |     |     |     | 795    |     |     |     |     |     | 800 |      |  |
| CTG | GCC | TTA | CCA | CCA | CGA | GCT | TAT | GCC | TAGTAA |     |     |     |     |     |     | 2433 |  |
| Leu | Ala | Leu | Pro | Pro | Arg | Ala | Tyr | Ala |        |     |     |     |     |     |     |      |  |
|     |     |     |     | 805 |     |     |     | 810 |        |     |     |     |     |     |     |      |  |

## (2) INFORMATION FOR SEQ ID NO: 50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ser | Thr | Asn | Pro | Lys | Pro | Gln | Arg | Lys | Thr | Lys | Arg | Asn | Thr | Asn |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Arg | Arg | Pro | Gln | Asp | Val | Lys | Phe | Pro | Gly | Gly | Gly | Gln | Ile | Val | Gly |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gly | Val | Tyr | Leu | Leu | Pro | Arg | Arg | Gly | Pro | Arg | Leu | Gly | Val | Arg | Ala |  |  |

| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Lys | Thr | Ser | Glu | Arg | Ser | Gln | Pro | Arg | Gly | Arg | Arg | Gln | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Pro | Lys | Ala | Arg | Arg | Pro | Glu | Gly | Arg | Ala | Trp | Ala | Gln | Pro | Gly |
|     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Tyr | Pro | Trp | Pro | Leu | Tyr | Gly | Asn | Glu | Gly | Met | Gly | Trp | Ala | Gly | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Leu | Ser | Pro | Arg | Gly | Ser | Arg | Pro | Ser | Trp | Gly | Pro | Thr | Asp | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Arg | Ser | Arg | Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Gly | Phe | Ala | Asp | Leu | Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Gly | Ala | Ala | Arg | Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Gly | Val | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Val | Arg | Asn | Val | Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Cys | Val | Pro | Cys | Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val |
|     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Ala | Leu | Thr | Pro | Thr | Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Ile | Arg | Arg | His | Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ala | Met | Tyr | Val | Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp |
|     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Asp | Met | Met | Met | Asn | Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser | Gln |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Leu | Arg | Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Trp | Gly | Val | Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly |     |

| 370        |            |            |            |            | 375        |            |            |            |            | 380        |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Thr<br>385 | Arg        | Val        | Ser        | Gly        | Gly<br>390 | Ala        | Ala        | Ala        | Ser        | Asp<br>395 | Thr        | Arg        | Gly        | Leu        | Val<br>400 |
| Ser        | Leu        | Phe        | Ser        | Pro<br>405 | Gly        | Ser        | Ala        | Gln        | Lys<br>410 | Ile        | Gln        | Leu        | Val        | Asn<br>415 | Thr        |
| Asn        | Gly        | Ser        | Trp<br>420 | His        | Ile        | Asn        | Arg        | Thr<br>425 | Ala        | Leu        | Asn        | Cys        | Asn<br>430 | Asp        | Ser        |
| Leu        | Gln        | Thr<br>435 | Gly        | Phe        | Phe        | Ala        | Ala<br>440 | Leu        | Phe        | Tyr        | Lys        | His<br>445 | Lys        | Phe        | Asn        |
| Ser        | Ser<br>450 | Gly        | Cys        | Pro        | Glu        | Arg<br>455 | Leu        | Ala        | Ser        | Cys        | Arg<br>460 | Ser        | Ile        | Asp        | Lys        |
| Phe<br>465 | Ala        | Gln        | Gly        | Trp        | Gly<br>470 | Pro        | Leu        | Thr        | Tyr        | Thr<br>475 | Glu        | Pro        | Asn        | Ser        | Ser<br>480 |
| Asp        | Gln        | Arg        | Pro        | Tyr<br>485 | Cys        | Trp        | His        | Tyr        | Ala<br>490 | Pro        | Arg        | Pro        | Cys        | Gly<br>495 | Ile        |
| Val        | Pro        | Ala        | Ser<br>500 | Gln        | Val        | Cys        | Gly        | Pro<br>505 | Val        | Tyr        | Cys        | Phe        | Thr<br>510 | Pro        | Ser        |
| Pro        | Val        | Val<br>515 | Val        | Gly        | Thr        | Thr        | Asp<br>520 | Arg        | Phe        | Gly        | Val        | Pro<br>525 | Thr        | Tyr        | Asn        |
| Trp<br>530 | Gly        | Ala        | Asn        | Asp        | Ser        | Asp<br>535 | Val        | Leu        | Ile        | Leu        | Asn<br>540 | Asn        | Thr        | Arg        | Pro        |
| Pro<br>545 | Arg        | Gly        | Asn        | Trp        | Phe<br>550 | Gly        | Cys        | Thr        | Trp        | Met<br>555 | Asn        | Gly        | Thr        | Gly        | Phe<br>560 |
| Thr        | Lys        | Thr        | Cys        | Gly<br>565 | Gly        | Pro        | Pro        | Cys        | Asn<br>570 | Ile        | Gly        | Gly        | Ala<br>575 | Gly        | Asn        |
| Asn        | Thr        | Leu        | Thr<br>580 | Cys        | Pro        | Thr        | Asp<br>585 | Cys        | Phe        | Arg        | Lys        | His        | Pro<br>590 | Glu        | Ala        |
| Thr        | Tyr<br>595 | Ala        | Arg        | Cys        | Gly        | Ser        | Gly<br>600 | Pro        | Trp        | Leu        | Thr        | Pro<br>605 | Arg        | Cys        | Met        |
| Val        | His<br>610 | Tyr        | Pro        | Tyr        | Arg        | Leu<br>615 | Trp        | His        | Tyr        | Pro        | Cys<br>620 | Thr        | Val        | Asn        | Phe        |
| Thr<br>625 | Ile        | Phe        | Lys        | Val        | Arg<br>630 | Met        | Tyr        | Val        | Gly        | Gly<br>635 | Val        | Glu        | His        | Arg        | Phe<br>640 |
| Glu        | Ala        | Ala        | Cys        | Asn<br>645 | Trp        | Thr        | Arg        | Gly        | Glu<br>650 | Arg        | Cys        | Asp        | Leu        | Glu<br>655 | Asp        |
| Arg        | Asp        | Arg        | Ser<br>660 | Glu        | Leu        | Ser        | Pro<br>665 | Leu        | Leu        | Leu        | Ser        | Thr        | Thr<br>670 | Glu        | Trp        |
| Gln        | Ile        | Leu<br>675 | Pro        | Cys        | Ser        | Phe        | Thr<br>680 | Thr        | Leu        | Pro        | Ala        | Leu<br>685 | Ser        | Thr        | Gly        |
| Leu<br>690 | Ile        | His        | Leu        | His        | Gln        | Asn<br>695 | Ile        | Val        | Asp        | Val        | Gln<br>700 | Tyr        | Leu        | Tyr        | Gly        |

Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu  
 705 710 715 720  
 Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp  
 725 730 735  
 Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val  
 740 745 750  
 Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe  
 755 760 765  
 Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro  
 770 775 780  
 Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu  
 785 790 795 800  
 Leu Ala Leu Pro Pro Arg Ala Tyr Ala  
 805

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys  
 1 5 10 15  
 Val

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..22

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 1 5 10 15

Ser Pro Thr Thr Ala Leu  
 20

## (2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1..37

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
 1 5 10 15

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr  
 20 25 30

Pro Gly Cys Gly Lys  
 35

## (2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1..25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr  
 1 5 10 15

Gln Leu Arg Arg His Ile Asp Leu Leu  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: Modified-site  
(B) LOCATION: 1..25

Gly Gly Thr Pro Thr Leu Ala Ala Arg Asp Ala Ser Val Pro Thr Thr  
1 5 10 15  
Thr Ile Arg Arg His Val Asp Leu Leu  
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
1          5          10          15

Ser Thr Gly Leu
          20

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro  
1 5 10 15  
Asn Ser Ser Ile  
20



## (2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asp | Cys | Pro | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | His | Asp | Ala | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | His | Thr | Pro |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Pro | Gly | Cys | Val |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Asp | Ala | Ile | Leu | His | Thr | Pro | Gly | Val | Pro | Cys | Val | Arg | Glu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn | Val | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro  
 1                      5                      10                      15  
 Thr Val Ala Thr  
                     20

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr  
 1                      5                      10                      15  
 Gln Leu Arg Arg  
                     20

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser  
 1                      5                      10                      15  
 Ala Thr Leu Cys  
                     20

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu             | Val | Gly | Ser | Ala | Thr | Leu | Cys | Ser | Ala | Leu | Tyr | Val | Gly | Asp | Leu |
| 1               |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Cys Gly Ser Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln             | Leu | Phe | Thr | Phe | Ser | Pro | Arg | Arg | His | Trp | Thr | Thr | Gln | Gly | Cys |
| 1               |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asn Cys Ser Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr             | Gln | Gly | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr | Gly | His |
| 1               |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg Met Ala Trp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear







(2) INFORMATION FOR SEQ ID NO: 77:

- (ii) MOLECULE TYPE: peptide

Gly Pro Asp Gln  
20

(ii) MOLECULE TYPE: peptide

Pro Lys Pro Cys  
20

(ii) MOLECULE TYPE: peptide

Cys Gly Pro Val

20

## (2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Ser | Val | Cys | Gly | Pro | Val | Tyr | Cys | Phe | Thr | Pro | Ser | Pro | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |
|-----|-----|-----|-----|
| Val | Val | Gly | Thr |
|     |     |     | 20  |

## (2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Ser | Gly | Ala | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |
|-----|-----|-----|-----|
| Tyr | Ser | Trp | Gly |
|     |     |     | 20  |

## (2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Pro | Thr | Tyr | Ser | Trp | Gly | Glu | Asn | Asp | Thr | Asp | Val | Phe | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |
|-----|-----|-----|-----|
| Leu | Asn | Asn | Thr |
|     |     |     | 20  |

## (2) INFORMATION FOR SEQ ID NO: 83:





- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly  
1 5 10 15

Ser Gly Pro Trp  
20

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp  
1 5 10 15

Tyr Pro Tyr Arg  
20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile  
1 5 10 15

Asn Tyr Thr Ile  
20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear



Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr Thr  
1 5 10 15  
Gln Trp Gln Val  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu  
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES







## (2) INFORMATION FOR SEQ ID NO: 105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:  
GCTCCATTGT GTATGAGGCA GCGG

24

## (2) INFORMATION FOR SEQ ID NO: 106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:  
GAGCTCCCGC TGCTGGGTAG CGC

23

## (2) INFORMATION FOR SEQ ID NO: 107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:  
CCTCCGTCCC CACCACGACA ATACG

25

## (2) INFORMATION FOR SEQ ID NO: 108:







## (2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
 1                      5                      10                      15  
 Ser Asn Ser Ser  
                     20

## (2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp  
 1                      5                      10                      15  
 Met Ile Met His Thr  
                     20

## (2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val  
 1                      5                      10                      15

Arg Glu Asn Asn Ser  
20

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu  
 1 5 10 15

Thr Pro Thr Leu Ala  
 20

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro  
 1 5 10 15

Thr Thr Thr Ile Arg  
 20

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser                 | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | Val | Asp | Leu | Leu | Val |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |
| Gly Ala Ala Ala Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu                 | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val | Gly |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |
| Asp Leu Cys Gly Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr                 | Val | Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |
| Phe Thr Ile Ser Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: peptide

Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln  
1 5 10 15

Asp Cys Asn Cys Ser  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr  
1 5 10 15

Gly His Arg Met Ala  
20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 1           5           10           15
Ser Pro Thr Thr Ala
                20

```